

FIG. 1

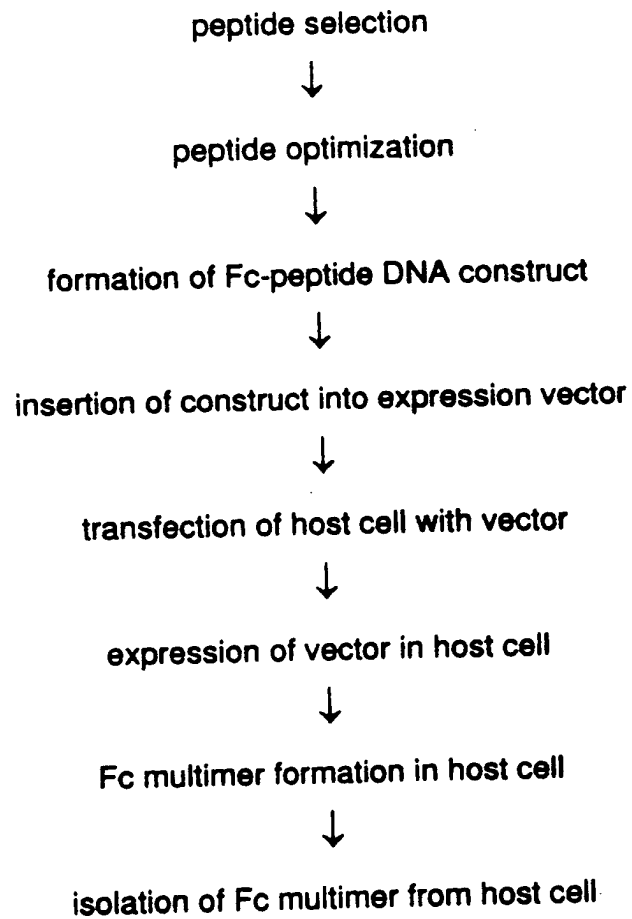


FIG. 2A

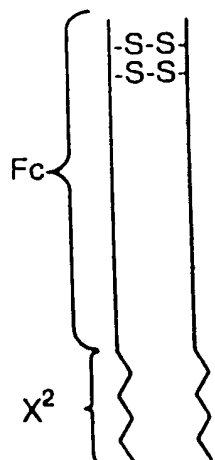


FIG. 2B

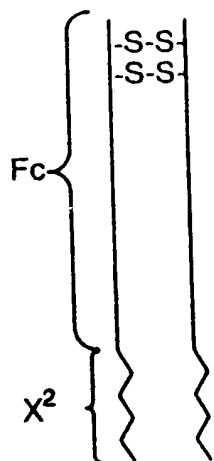


FIG. 2C

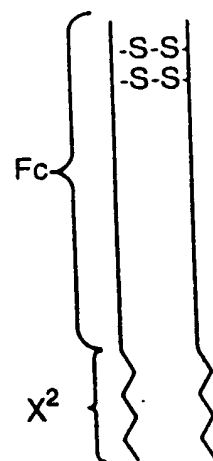


FIG. 2D

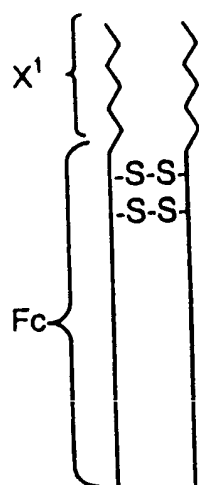


FIG. 2E

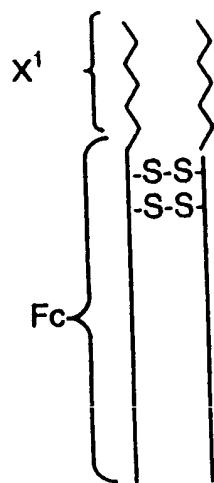


FIG. 2F

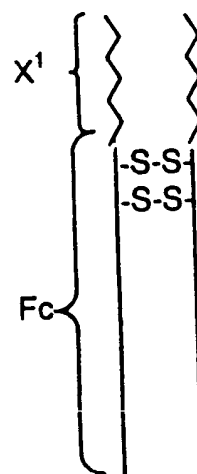


FIG. 3A

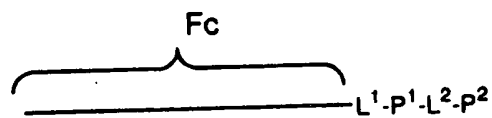


FIG. 3B

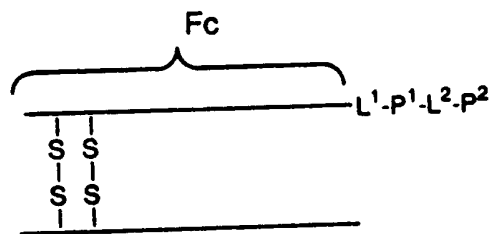


FIG. 3C

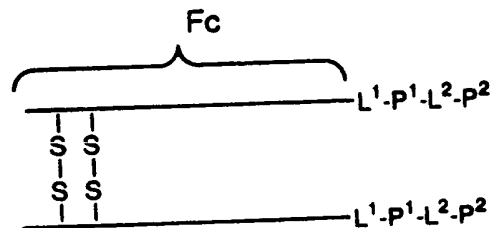


FIG. 5

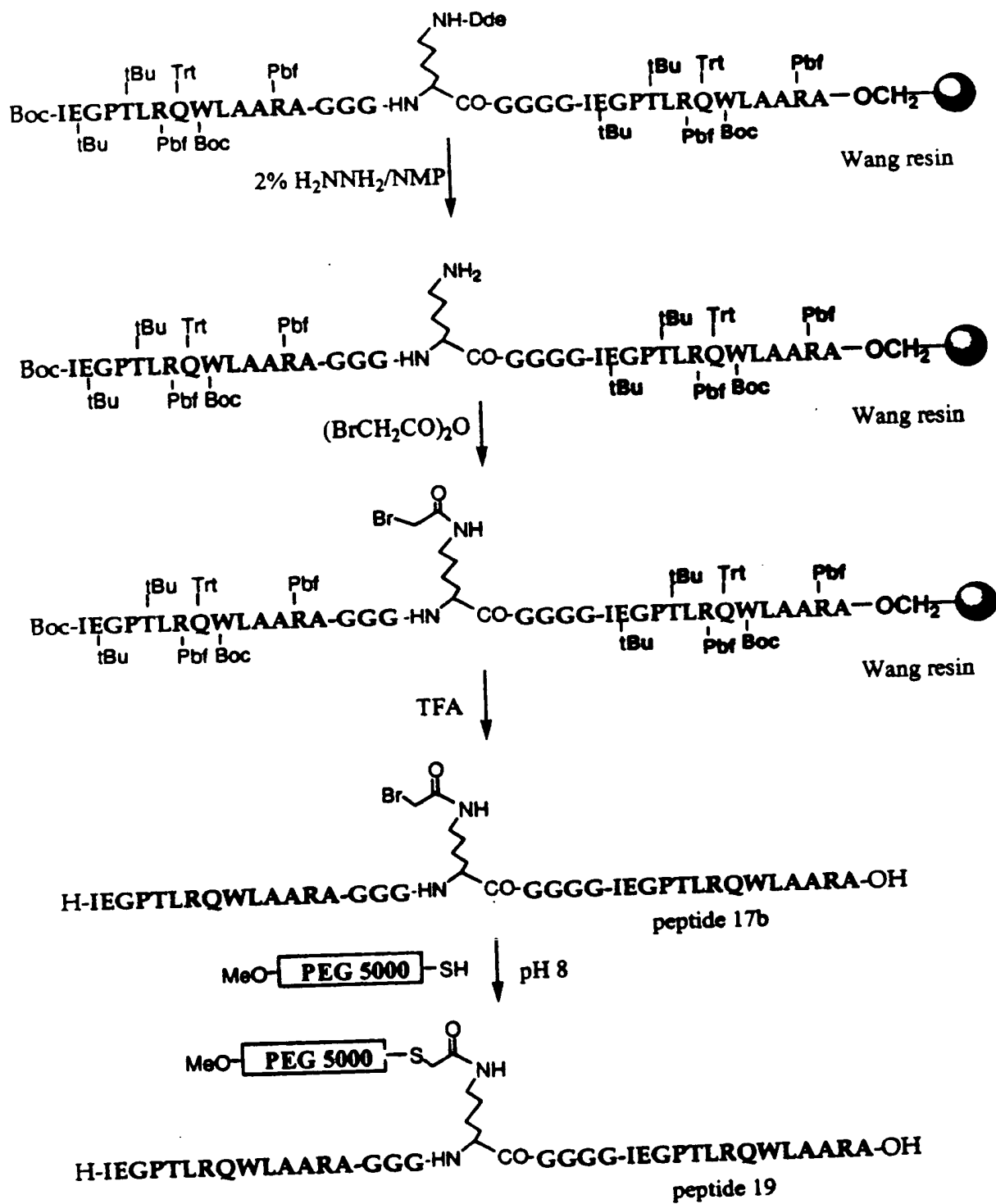


FIG. 6

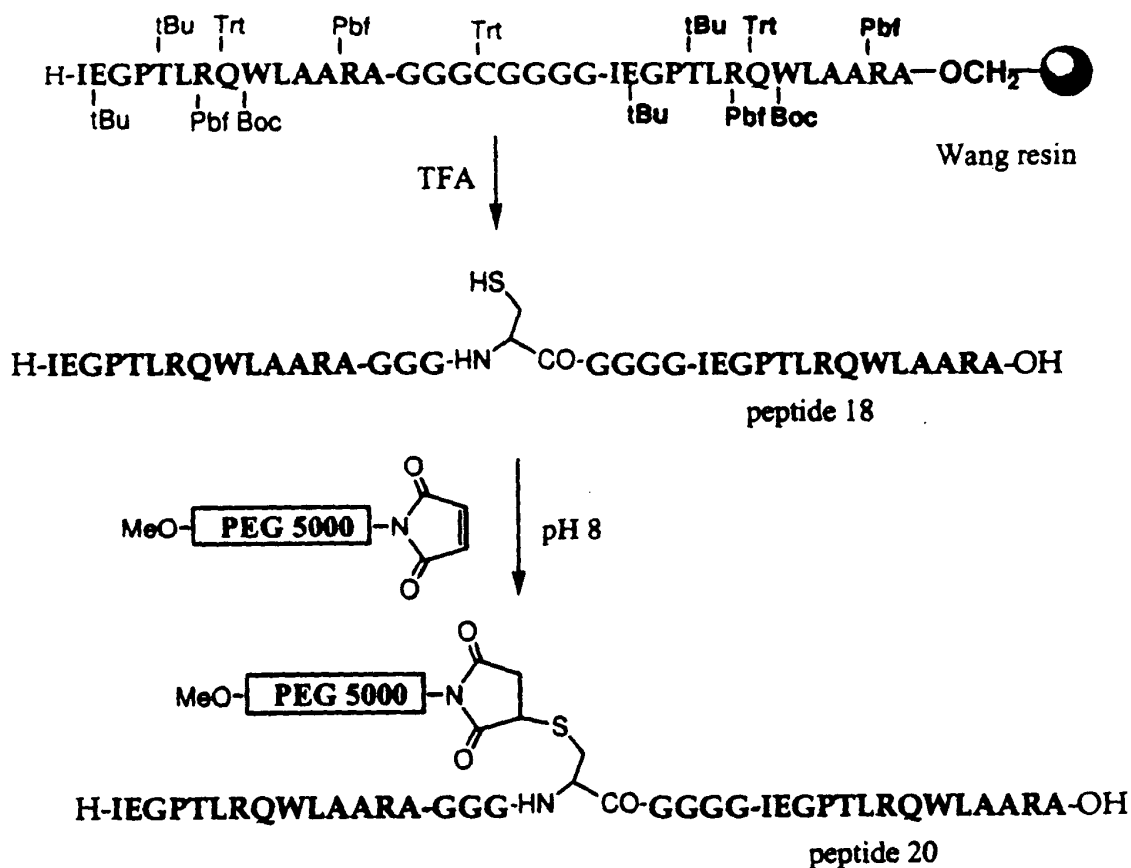


FIG. 8

XbaI
|
1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC 60
AGATCTAAACAAAATTGATTAATTTCTCCTTATTGTATACCTGTTTGTAGTGTGTACAG
M D K T H T C P -
C
CACCTTGTCAGCTCCGGAACCTCTGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAAC
61 GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGTTTG 120
P C P A P E L L G G P S V F L F P P K P -
C
CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
121 GGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT 180
K D T L M I S R T P E V T C V V V D V S -
C
GCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
181 CCGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC 240
H E D P E V K F N W Y V D G V E V H N A -
C
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCA
241 GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT 300
K T K P R E E Q Y N S T Y R V V S V L T -
C
CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
301 GGCAGGACGTGGTCTGACCGACTTACCGTTCCTCATGTTACGTTCCAGAGGTTGTTTC 360
V L H Q D W L N G K E Y K C K V S N K A -
C
CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGGAGCCCCGAGAACCAC
361 GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG 420
L P A P I E K T I S K A K G Q P R E P Q -
C
AGGTGTACACCTGCCCCCATCCCCGGATGAGCTGACCAAGAACCAGGTACGCCTGACCT
421 TCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA 480
V Y T L P P S R D E L T K N Q V S L T C -
C
GCCTGGTCAAAGCCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
481 CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTGCG 540
L V K G F Y P S D I A V E W E S N G Q P -
C
CGGAGAACAACCTACAAGACCACGCCTCCCGTGGTGGACTCCGACGGCTCCTTCTCTCTCT
541 GCCTCTTGTGTGATGTTCTGGTGGGAGGGCAGACCTGAGGCTGCCGAGGAAGAAGGAGA 600
E N N Y K T T P P V L D S D G S F F L Y -
C
ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
601 TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCTTTCGAGAAGAGTACGAGGC 660
S K L T V D K S R W Q Q G N V F S C S V -
C
TGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGGTA
661 ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGGCCCAT 720
M H E A L H N H Y T Q K S L S L S P G K -
C
AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCTG
721 TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTCACCGACCGAGCAGCAGCAG 780
G G G G G I E G P T L R Q W L A A R A G -
C
GTGGTGGAGGTGGCGGGGAGGTATTGAGGGCCCAACCTTCGCCAATGGCTTGCAGCAC
781 CACCACCTCCACCGCGCTCCATAACTCCCGGTTGGGAAGCGGTTACCGAACGTCTGTG 840
G G G G G G I E G P T L R Q W L A A R -
C
BamHI
|
CGGCATAATCTCGAGGATCCG
841 CGCGTATTAGAGCTCCTAGGC 861
C A * -

FIG. 9

XbaI
|
1 TCTAGATTTGTTTAACTAATTAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC 60
AGATCTAAACAAAATTGATTAATTCCTCTTATTGTATACTAGCTTCCAGGCTGAGACG
M I E G P T L R
c
GTCAGTGGCTGGCTGCTCGTGCTGGCGGTGGTGGCGGAGGGGGTGGCATTGAGGGCCCAA
61 CAGTCACCGACCGACGAGCAGCAGCCACCACCGCCTCCCCACCGTAACCTCCGGGTT 120
Q W L A A R A G G G G G G G G I E G P T
c
CCCTTCGCCAATGGCTTGACGACGCGCAGGGGGAGGCGGTGGGGACAAAACCTCACACAT
121 GGGAAAGCGGTTACCGAACGTCGTGCGCGTCCCCCTCCGCCACCCCTGTTTGTAGTGTGA 180
L R Q W L A A R A G G G G G G D K T H T C
c
GTCCACCTTGCCAGCACCTGAACCTCGGGGGACCGTCAGTTTCTCTTCCCCCAA
181 CAGGTGGAACGGGTGCTGGACTTGAGGACCCCCCTGGCAGTCAAAGGAGAAGGGGGGTT 240
P P C P A P E L L G G P S V F L F P P K
c
AACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACG
241 TTGGGTTCTGTGGAGTACTAGAGGGCCTGGGACTCCAGTGTACGCACCAACACCTGC 300
P K D T L M I S R T P E V T C V V V D V
c
TGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATA
301 ACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTAT 360
S H E D P E V K F N W Y V D G V E V H N
c
ATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAGCGTCC
361 TACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGTCGTCATGGCACACCACTGCGAGG 420
A K T K P R E E Q Y N S T Y R V V S V L
c
TCACCGTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAACA
421 AGTGGCAGGACGTGGTCTGACCGACTTACCGTTCTCTCATGTTACGTTCCAGAGGTTGT 480
T V L H Q D W L N G K E Y K C K V S N K
c
AAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC
481 TTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTG 540
A L P A P I E K T I S K A K G Q P R E P
c
CACAGGTGTACACCTGCCGCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGA
541 GTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCCGACT 600
Q V Y T L P P S R D E L T K N Q V S L T
c
CCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC
601 GGACGGACCAAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCG 660
C L V K G F Y P S D I A V E W E S N G Q
c
AGCCGGAGAACAACATAAGACCACGCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC
661 TCGGCTCTTGTGATGTTCTGGTGGCGAGGGCAGACCTGAGGCTGCCGAGGAAGAAGG 720
P E N N Y K T T P P V L D S D G S F P L
c
TCTACAGCAAGCTCACCGTGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCT
721 AGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCTTGCAGAAGAGTACGA 780
Y S K L T V D K S R W Q Q G N V F S C S
c
CCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
781 GGCACCTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCC 840
V M H E A L H N H Y T Q K S L S L S P G
c
BamHI
|
841 GTAAATAATGGATCC 855
CATTATTACCTAGG
K *

FIG. 10

XbaI
|
1 TCTAGATTGTTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC 60
AGATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACTAGCTTCCAGGCTGAGACG
M I E G P T L R -

61 GTCAGTGGCTGGCTGCTCGTGGTGGAGGCGGTGGGGACAAACTCACACATGTCCAC 120
CAGTCACCGACCGACGAGCAGCACCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTG
Q W L A A R A G G G G G D K T H T C P P -

121 CTTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTCTCTCTCCCCCAAAACCCA 180
GAACGGGTGCTGGACTTGAGGACCCCTGGCAGTCAAAGGAGAAGGGGGTTTTGGGT
C P A P E L L G G P S V F L F P P K P K -

181 AGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCC 240
TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCCACCACCACCTGCCTCGG
D T L M I S R T P E V T C V V V D V S H -

241 ACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA 300
TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGACCTCCACGTATTACGGT
E D P E V K F N W Y V D G V E V H N A K -

301 AGACAAAGCCCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCCAGCGTCTCACCG 360
TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC
T K P R E E Q Y N S T Y R V V S V L T V -

361 TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGCCC 420
AGGACGTGGTCTGACCGACTTACCGTTCCCTCATGTTCCAGTTCAGAGGTTGTTTCGGG
L H Q D W L N G K E Y K C K V S N K A L -

421 TCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG 480
AGGGTCCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCC
P A P I E K T I S K A K G Q P R E P Q V -

481 TGTACACCCCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTACGCTGACCTGCC 540
ACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGG
Y T L P P S R D E L T K N Q V S L T C L -

541 TGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG 600
ACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCCGGCC
V K G F Y P S D I A V E W E S N G Q P E -

601 AGAACAACCTACAAGACCACGCCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACA 660
TCTTGTGATGTTCTGGTCCGGAGGGCAGCACCTGAGGCTGCCGAGGAAGAAGGAGATGT
N N Y K T T P P V L D S D G S F F L Y S -

661 GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA 720
CGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGCACT
K L T V D K S R W Q Q G N V F S C S V M -

721 TGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGGTAAAT 780
ACGTACTCCGAGACGTGTTGGTGTGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTA
H E A L H N H Y T Q K S L S L S P G K * -

BamHI
|
AATGGATCC
781 TTACCTAGG

FIG.11

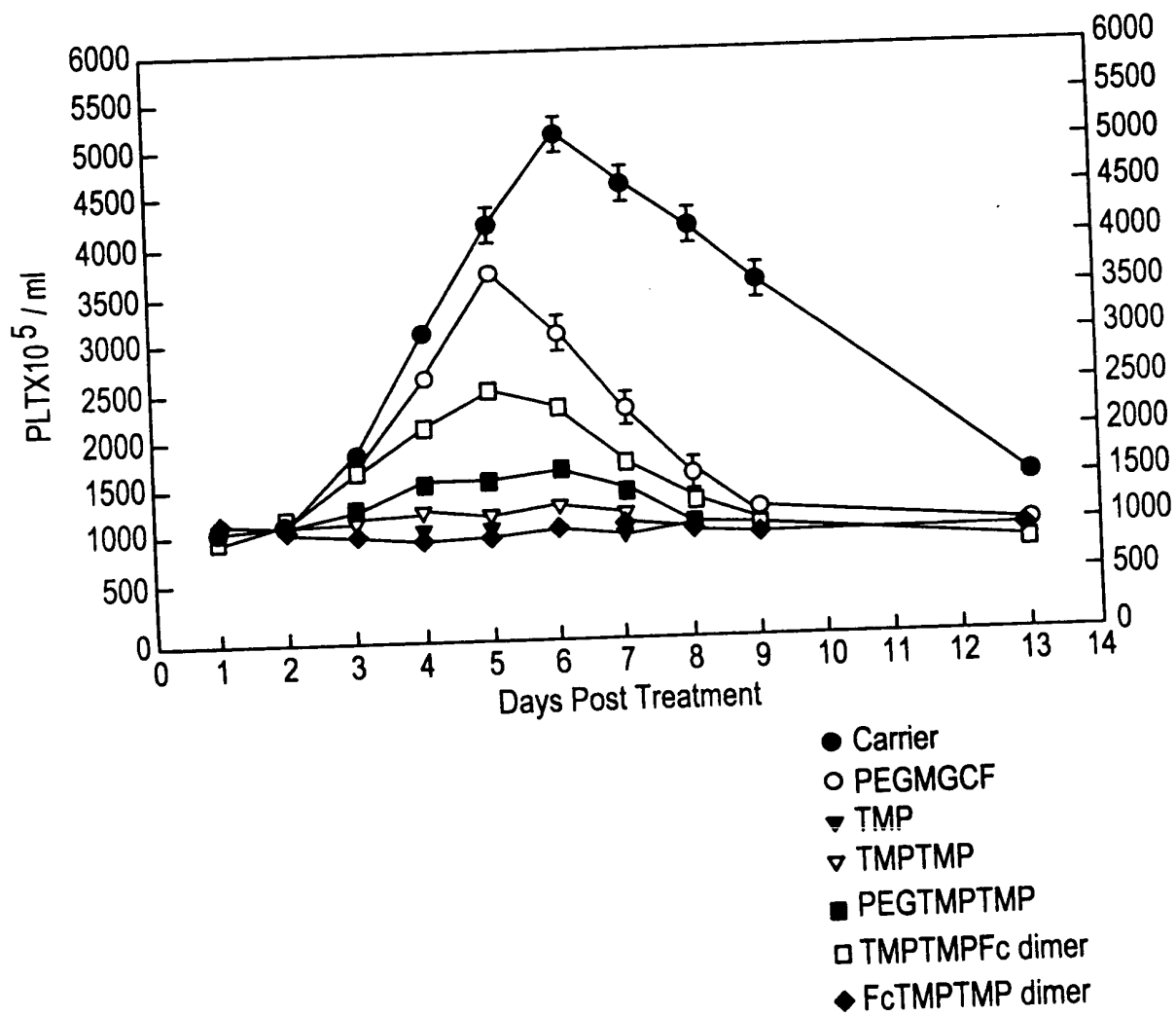
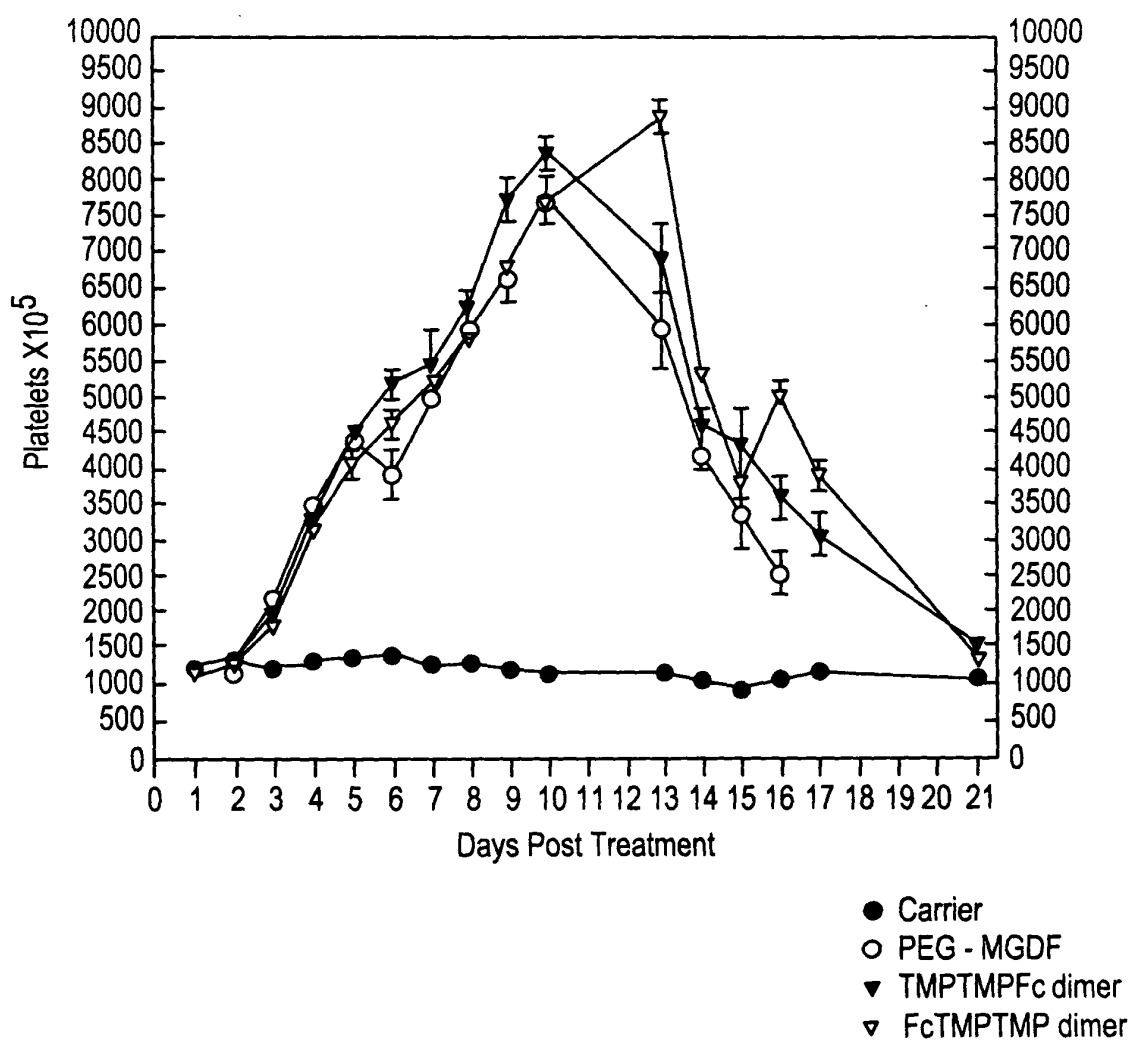


FIG.12



C

FIG. 14

XbaI
|
1 TCTAGATTGTTTAACTAATTAAAGGAGGAATAACATATGGGAGGTACTTACTCTTGCC 60
AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCCTCCATGAATGAGAACGG
M G G T Y S C H
c
61 ACTTCGGCCCCGCTGACTTGGGTATGTAAGCCACAAGGGGGTGGGGGAGGCGGGGGGACA 120
TGAAGCCGGGCGACTGAACCCATACATTGGGTGTTCCCCCACCCTCCGCCCCCTGT
F G P L T W V C K P Q G G G G G G G D K
c
121 AAACCTCACACATGTCCACCTTGCCAGCACCTGAACCTCCTGGGGGACCGTCAGTTTTCC 180
TTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCTGGCAGTCAAAAGG
T H T C P P C P A P E L L G G P S V F L
c
181 TCTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAACATGCG 240
AGAAGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGACTCCAGTGTACGC
P P P K P K D T L M I S R T P E V T C V
c
241 TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 300
ACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGC
V V D V S H E D P E V K F N W Y V D G V
c
301 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGTACCGTG 360
ACCTCCACGTATTACGGTTCTGTTCGGCGCCCTCCTCGTCATGTTGTGTCATGGCAC
E V H N A K T K P R E E Q Y N S T Y R V
c
361 TGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGCCAAGGAGTACAAGTGCA 420
ACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTCATGTTACAGT
V S V L T V L H Q D W L N G K E Y K C K
c
421 AGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGC 480
TCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCG
V S N K A L P A P I E K T I S K A K G Q
c
481 AGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACC 540
TCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTCTTGG
P R E P Q V Y T L P P S R D E L T K N Q
c
541 AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGG 600
TCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTTCGCTGTAGCGGCACCTCACCC
V S L T C L V K G F Y P S D I A V E W E
c
601 AGAGCAATGGGCAGCCGGAGAACAACATAAGACCACGCCTCCCGTGCTGGACTCCGACG 660
TCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGCGACACCTGAGGCTGC
S N G Q P E N N Y K T T P P V L D S D G
c
661 GCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG 720
CGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCTTGGC
S F F L Y S K L T V D K S R W Q Q G N V
c
721 TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT 780
AGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTATGCGCTCTTCTCGGAGA
F S C S V M H E A L H N H Y T Q K S L S
c
BamHI
|
781 CCCTGTCTCCGGTAAATAATGGATCC 807
GGGACAGAGGCCCATTTATTACCTAGG
L S P G K *

FIG. 15

XbaI
|

1 TCTAGATTTGAGTTTTAACTTTTGAAGGAGGAATAAAATATGGGAGGTACTTACTCTTG 60
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b AGATCTAAACTCAAATGAAAATCTTCCTCCTTATTTTATACCTCCATGAATGAGAAC
M G G T Y S C -

61 CCACTTCGGCCCACTGACTTGGGTTTGCAAAACCGCAGGGTGGCGGGCGCGCGCGGTGG 120
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b GGTGAAGCCGGGTGACTGAACCCAAACGTTTGGCGTCCACCGCGCGCGCGCGCGCCACC
H F G P L T W V C K P Q G G G G G G G G -

121 TACCTATTCTGTCTATTTTGGCCCGCTGACCTGGGTATGTAAGCCACAAGGGGGTGGGGG 180
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b ATGGATAAGGACAGTAAAACCGGCGGACTGGACCCATACATTTCGGTGTTCCTCCACCCCC
T Y S C H F G P L T W V C K P Q G G G G -

181 AGGCGGGGGGGACAAAACCTCACACATGTCCACCTTGCCACGACCTGAACTCTCGGGGG 240
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b TCCGCCCCCCTGTTTGTAGTGTGTACAGGTGGAACGGGTCTGTGGACTTGAGGACCCCC
G G G D K T H T C P P C P A P E L L G G -

241 ACCGTCAAGTTTCTCTTCCCCCAAACCCAAGGACACCTCATGATCTCCCGGACCCC 300
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b TGGCAGTCAAAAGGAGAAGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGG
P S V F L F P P K P K D T L M I S R T P -

301 TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTG 360
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b ACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGAC
E V T C V V V D V S H E D P E V K F N W -

361 GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAGCCGCGGGAGGAGCAGTACAA 420
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b CATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTT
Y V D G V E V H N A K T K P R E E Q Y N -

421 CAGCACGTACCGTGTGGTCAGCGTCTCACCCTGCTGCACCAGGACTGGCTGAATGGCAA 480
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b GTCGTGCATGGCACACCAGTGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTT
S T Y R V V S V L T V L H Q D W L N G K -

481 GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTC 540
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b CCTCATGTTTACGTTCCAGAGGTTGTTTGGGAGGGTGGGGGTAGCTCTTTTGGTAGAG
E Y K C K V S N K A L P A P I E K T I S -

541 CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGA 600
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b GTTTCGGTTTCCCGTCCGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACT
K A K G Q P R E P Q V Y T L P P S R D E -

601 GCTGACCAAGAACCAGGTGACCTGCTGGTCAAAGGCTTCTATCCACGCGACAT 660
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b CGACTGGTTCTTGGTCCAGTCCGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTA
L T K N Q V S L T C L V K G F Y P S D I -

661 CGCCGTGGAGTGGGAGAGCAATGGCCAGCCGAGAACAACATAAGACCACGCTCCCGT 720
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b GCGGCACCTCACCTCTCGTTACCGCTCGGCCTCTTGTGTATGTTCTGGTGGCGAGGGCA
A V E W E S N G Q P E N N Y K T T P P V -

721 GCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG 780
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b CGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCAGTGGACCTGTTCTCGTCCAC
L D S D G S F F L Y S K L T V D K S R W -

781 GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC 840
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b CGTCGTCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTG
Q Q G N V F S C S V M H E A L H N H Y T -

BamHI
|

841 GCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC 881
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
b CGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
O K S L S L S P G K -

FIG. 16

XbaI
|
1 TCTAGATTTGTTTAACTAATTAAGGAGGAATAACATATGGACAAAACCTCACACATGTC 60
AGATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACCTGTTTGGAGTGTGTACAG
M D K T H T C P -

61 CACCTTGCCCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTCCTCTTCCCCCAAAC 120
GTGGAACGGGTCGTGGACTTGAGGACCCCTGGCAGTCAAAAGGAGAAGGGGGTTTTC
P C P A P E L L G G P S V F L P P K P -

121 CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGGACGTGA 180
GGTTCCTGTGGAGTACTAGAGGGCCTGGGACTCCAGTGTACGCACCACCACCTGCCT
K D T L M I S R T P E V T C V V V D V S -

181 GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCAGTATTAC
H E D P E V K F N W Y V D G V E V H N A -

241 CCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAGCGTCTCTCA 300
GGTTCGTGTTTCGGCGCCCTCCTCGTCATGTTGTGTCATGGCACACCAGTCGCAGGAGT
K T K P R E E Q Y N S T Y R V V S V L T -

301 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG 360
GGCAGGACGTGCTCCTGACCGACTTACCGTTCCTCATGTTACGTTCCAGAGGTGTTTC
V L H Q D W L N G K E Y K C K V S N K A -

361 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCAC 420
GGGAGGGTCGGGGTAGTCTTTTGGTAGAGGTTTCGGTTTCCTCGTGGGGCTCTTGGTG
L P A P I E K T I S K A K G Q P R E P Q -

421 AGGTGTACACCCTGCCTCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT 480
TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTTCCTGGTCCAGTCGGACTGGA
V Y T L P P S R D E L T K N Q V S L T C -

481 GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG
L V K G P Y P S D I A V E W E S N G Q P -

541 CGGAGAACAACCTACAAGACACCGCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCT 600
GCCTCTGTGTTGATGTTCTGGTGGGAGGGCAGCTGAGGCTGCCGAGGAAGAAGGAGA
E N N Y K T T P P V L D S D G S F P L Y -

601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG 660
TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC
S K L T V D K S R W Q Q G N V F S C S V -

661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTA 720
ACTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCAT
M H E A L H N H Y T Q K S L S L S P G K -

721 AAGGTGGAGGTGGTGGCGGAGTACTTACTCTTGCCACTTCGGCCCACTGACTTGGGTTT 780
TTCCACCTCCACCACCGCTCCATGAATGAGAACGGTGAAGCCGGGTGACTGAACCCAAA
G G G G G G G T Y S C H F G P L T W V C -

781 GCAAACCGCAGGGTGGCGGGCGGGCGGGTGGTACCTATTCTGTCAATTTGGCCCCG 840
CGTTTGGCGTCCCACCGCGCGCGCGCCGCCACCATGGATAAGGACAGTAAACCGGGCG
K P Q G G G G G G G T Y S C H F G P L -

BamHI
|
841 TGACCTGGGTATGTAAGCCACAAGGGGGTTAATCTCGAGGATCC 884
ACTGGACCCATACATTCCGGTGTCCCCCAATTAGAGCTCCTAGG
T W V C K P Q G G *

FIG. 17A

[AatII sticky end] 5' GCGTAACGTATGCATGGTCTCC-
(position #4358 in pAMG21) 3' TGCACGCATTGCATACGTACCAGAGG-

- CCATGCGAGAGTAGGGAACTGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT -
- GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGA -
- GGGCCTTTTCGTTTTATCTGTTGTTTGTGCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC -
- CCCGGAAAGCAAATAGACAACAAACAGCCACTTGCGAGAGGACTCATCCTGTTTAGGCG -
- CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCCG -
- GCCCTCGCTAAACTTGCAACGCTTCGTTGCCGGGCCTCCACCGCCCGTCTGCGGGCG -
- CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTCGCT -
- GTATTTGACGGTCCGTAGTTTAATTCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA -
AatII
- TTCTACAACTCTTTTGTTTATTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC -
- AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG -
- TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAATGCTTTAGAAATACTTTGGCAGC -
- AAAATTTTCATACCCGTTAGTTAACGAGGACAATTTTAACGAAATCTTTATGAAACCGTCG -
- GGTGTGTTGATTGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCGCTTAC -
- CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTACTGGCACGCGAATG -
- TACAGCCTAATATTTTGAATATCCCAAGAGCTTTTTCCTTCGCATGCCACGCTAAAC -
- ATGTCGGATTATAAAAACTTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTTG -
- ATTCTTTTTCTCTTTTGGTTAAATCGTTGTTTGATTTATTATTTGCTATATTTATTTTC -
- TAAGAAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAACGATATAAATAAAAAAG -
- GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTCATACACGCATGTAAAAATA -
- CTATTAATAGTTGATCTCTTCCTTGTTAATTACCATACAAGTATGTGCGTACATTTTTAT -
- AACTATCTATATAGTTGTCTTCTCTGAATGTGCAAACTAAGCATTCCGAAGCCATTAT -
- TTGATAGATATATCAACAGAAAGAGACTTACACGTTTGTATTCGTAAGGCTTCGGTAATA -
- TAGCAGTATGAATAGGGAACTAAACCCAGTGATAAGACCTGATGATTTTCGCTTCTTTAA -
- ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAATT -
- TTACATTTGGAGATTTTATTTTACAGCATTGTTTTCAAATATATTCCAATTAATCGGTG -
- AATGTAAACCTCTAAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC -
- AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT -
- TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAATAATTTAATCGCAGTAGTA -
- AATATTGCCTCCATTTTATAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG -
- TTATAACGGAGGTAAAAATCCCATTAATAGGTCTTAACCTTTATAGTCTAAATTGGTATC -
- AATGAGGATAAATGATCGCGAGTAAATAATATTCACAAATGTACCATTTTAGTCATATCAG -
- TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTTACATGGTAAATCAGTATAGTC -
- ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTAAATTTTATTAATTATTCTGT -
- TATTCGTAACATAATTATAGTAATAACGAAGATGTCCGAAATTAAATAATTAATAAGACA -
- AAGTGTCGTCGGCATTTATGCTTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTG -
- TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG -
- GCAAGTTTTGCGTGTTATATATCATTAAACGGTAATAGATTGACATTTGATTCTAATAA -
- CGTTCAAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAACTAAGATTATT -

FIG. 17B

- ATTGGATTTTGTGTCACACTATTATATCGCTTGAAATACAATTGTTTAAACATAAGTACCTG -
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC -

- TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTTGATT -
- ATCCTAGCATGTCCAAATGCGTTCCTTTACCAAACAATATCAGCTAATTAGCTAAACTAA -

- CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA -
- GATCTAAACAAAATTGATTAATTTCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT -

- GCTCACTAGTGTGCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA -
- CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT -

- GAAGAAGAAGAAGAAAGCCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA -
- CTTCTTCTTCTTCTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT -

- ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTTGCTGAAAGGAGG -
- TGATCGTATTGGGGAACCCCGGAGATTGCCCAGAACTCCCCAAAAACGACTTTCCTCC -

- AACCGCTCTTCACGCTCTTCACGC 3' [SacII sticky end]
- TTGGCGAGAAGTGCGAGAAGTG 5' (position #5904 in pAMG21)

FIG.18A - 1

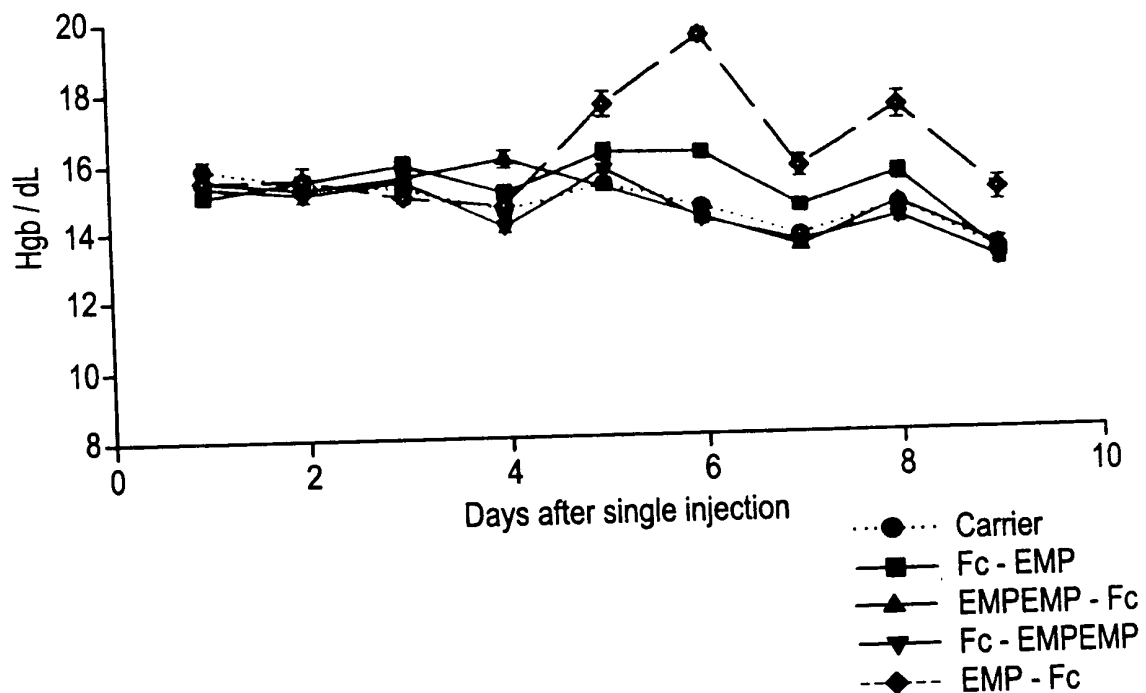


FIG.18A - 2

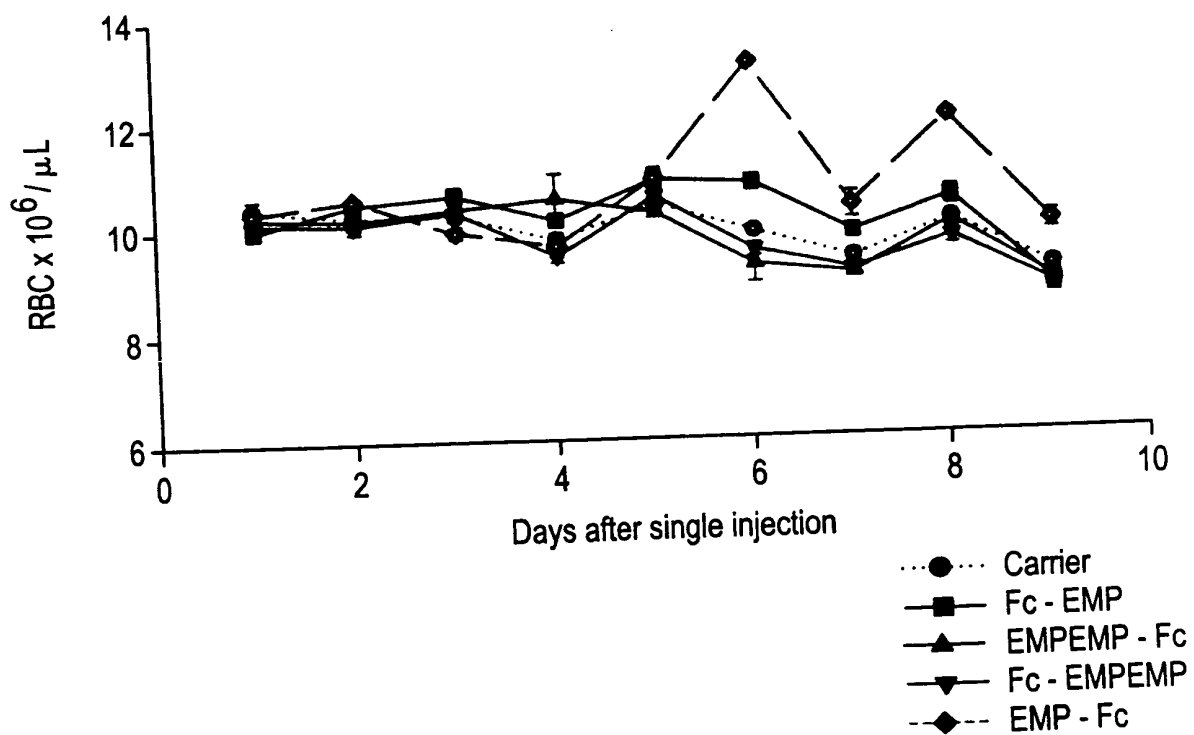


FIG.18A - 3

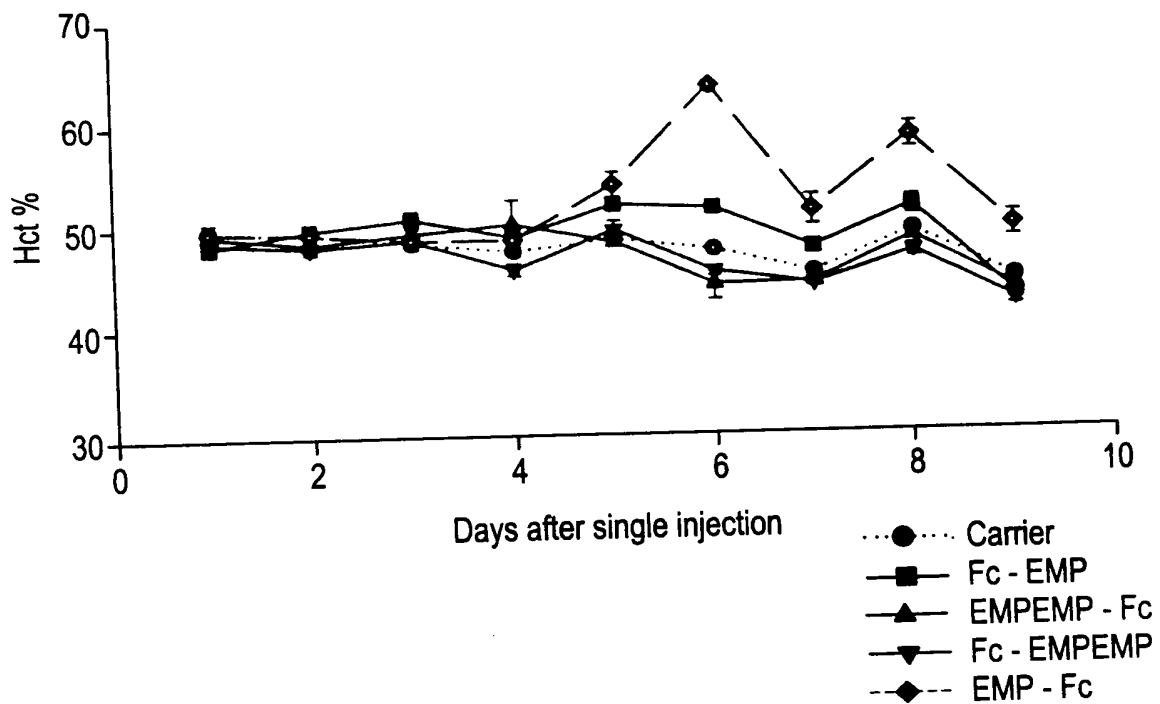


FIG.18B - 1

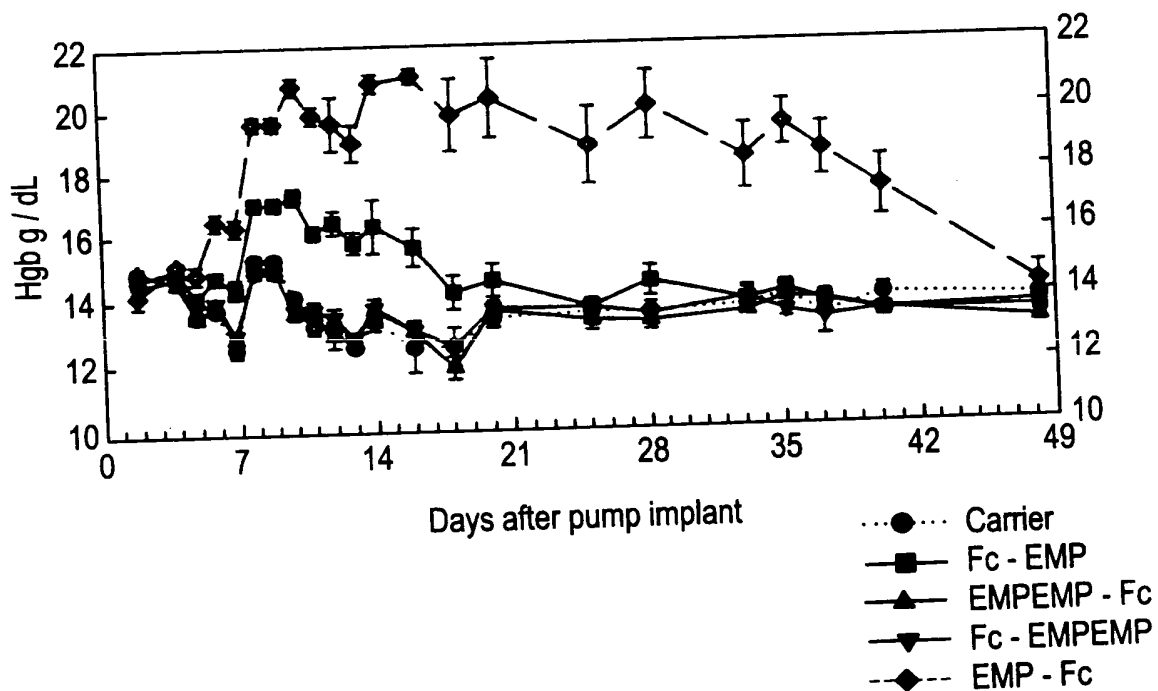


FIG.18B - 2

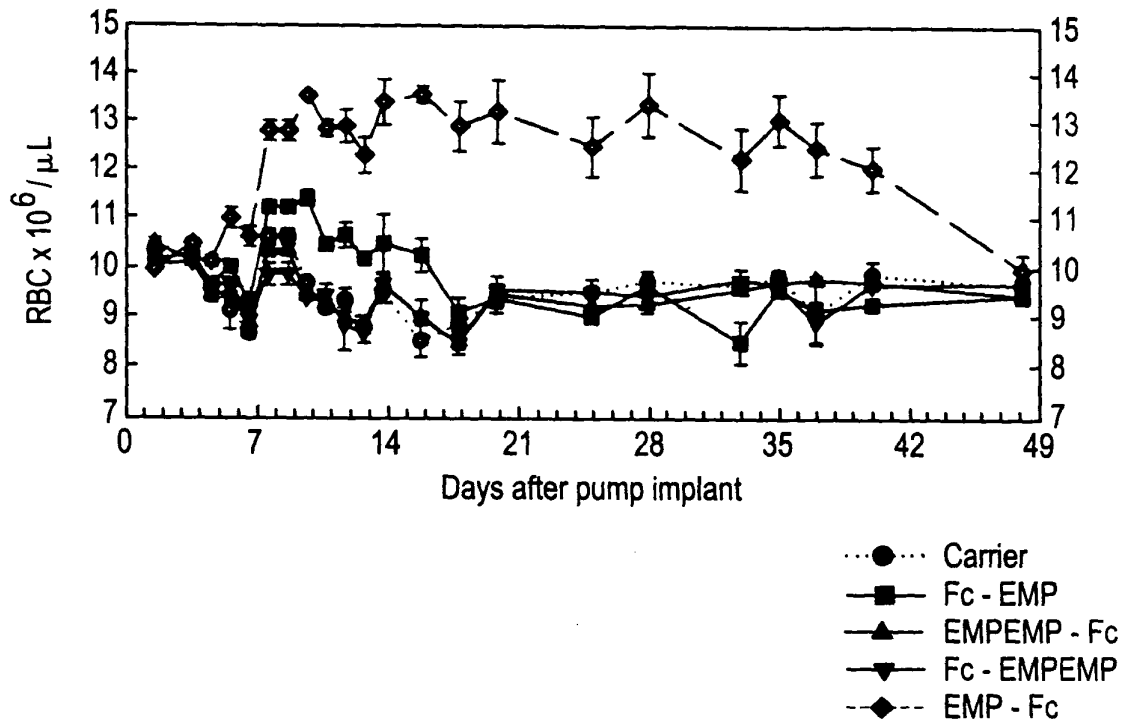


FIG.18B - 3

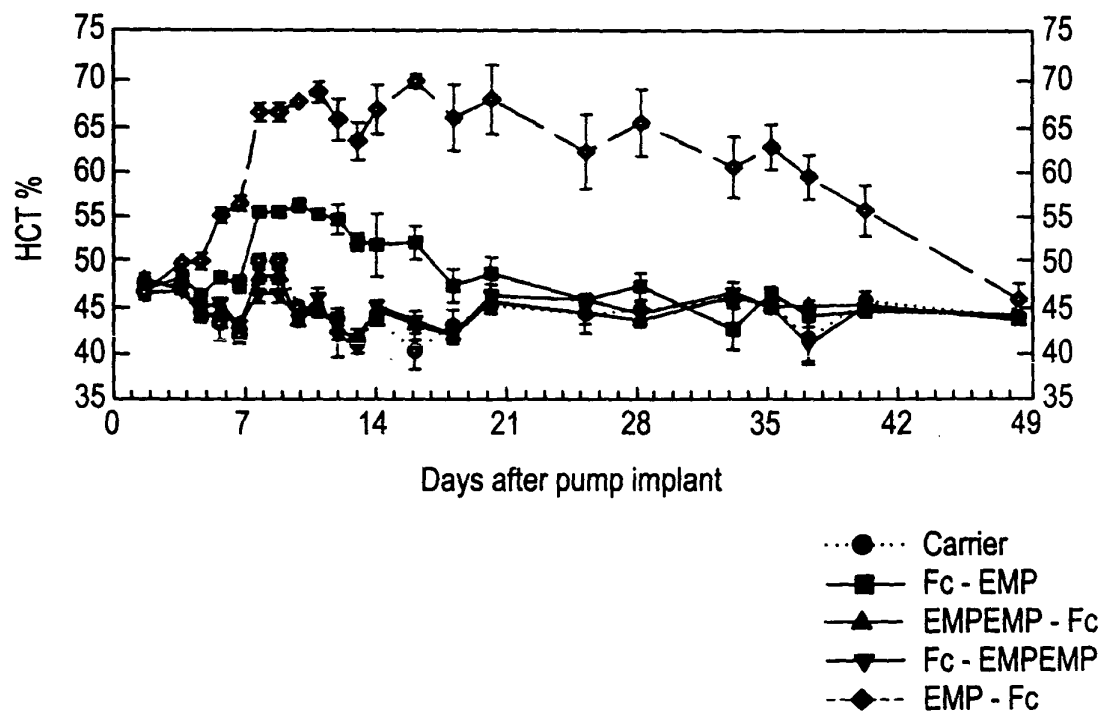


FIG. 19A

NdeI
|
1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG
-----+-----+-----+-----+-----+ 60
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
61 TCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
-----+-----+-----+-----+-----+ 120
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
-----+-----+-----+-----+-----+ 180
CAGTGACGCACCAACCACTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
-----+-----+-----+-----+-----+ 240
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC
a V D G V E V H N A K T K P R E E Q Y N S -
241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
-----+-----+-----+-----+-----+ 300
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA
-----+-----+-----+-----+-----+ 360
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGTTT
a Y K C K V S N K A L P A P I E K T I S K -
361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
-----+-----+-----+-----+-----+ 420
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
-----+-----+-----+-----+-----+ 480
TGGTTCCTGGTCCAGTCGGACTGGACGGACCAAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACATAAGACCACGCCTCCCGTGCTG
-----+-----+-----+-----+-----+ 540
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAGCAG
a V E W E S N G Q P E N N Y K T T P P V L -
541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+ 600
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 19B

```

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   .

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC
-----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCACTGAAGGACGGCGTGATG

a   K   S   L   S   L   S   P   G   K   G   G   G   G   G   D   F   L   P   H   Y   .

                                     BamHI
                                     |
721 AAAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC
-----+-----+-----+-----+-----+ 757
TTTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG

a   K   N   T   S   L   G   H   R   P   *
```

[illegible]

FIG. 20B

```

601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+ 660
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a   D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+ 720
GTCCCCTTGCAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG
-----+-----+-----+-----+ 761
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC

a   K S L S L S P G K *
```

FIG. 21A

NdeI
|
CATATGGACAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

TCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
61 -----+-----+-----+-----+-----+-----+-----+ 120
AGTCAGAAGGAGAAGGGGGTGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
121 -----+-----+-----+-----+-----+-----+-----+ 180
CAGTGACGACACCACCTGCACCTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
181 -----+-----+-----+-----+-----+-----+-----+ 240
CACCTGCCGCACCTCCACGTATTACGGTTCGTTCGCGGCCCTCCTCGTCATGTTGTGCG

a V D G V E V H N A K T K P R E E Q Y N S -

ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
241 -----+-----+-----+-----+-----+-----+-----+ 300
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
301 -----+-----+-----+-----+-----+-----+-----+ 360
ATGTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
361 -----+-----+-----+-----+-----+-----+-----+ 420
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

ACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
421 -----+-----+-----+-----+-----+-----+-----+ 480
TGGTTCCTTGGTCCAGTCGGACTGGACGGACAGTTTCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
481 -----+-----+-----+-----+-----+-----+-----+ 540
CACCTCACCCCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 21B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCTGAATGGACCCCGGGT
-----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA

a      K  S  L  S  L  S  P  G  K  G  G  G  G  G  F  E  W  T  P  G  -

                                     BamHI
                                     |
721 TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
-----+-----+-----+-----+-----+ 763
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC

a      Y  W  Q  P  Y  A  L  P  L  *
```

FIG. 22A

NdeI
|
CATATGTTCTGAATGGACCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG
a M F E W T P G Y W Q P Y A L P L G G G -
GGTGGGGACAAAACCTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG
61 -----+-----+-----+-----+-----+-----+-----+ 120
CCACCCCTGTTTGTAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCTGGC
a G G D K T H T C P P C P A P E L L G G P -
TCAGTTTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAG
121 -----+-----+-----+-----+-----+-----+-----+ 180
AGTCAAAAAGGAGAAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTAC
181 -----+-----+-----+-----+-----+-----+-----+ 240
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
241 -----+-----+-----+-----+-----+-----+-----+ 300
CACCTGCCGCACCTCCACGTATTACGGTTCGTGTTTCGGCGCCCTCCTCGTCATGTTGTGC
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
301 -----+-----+-----+-----+-----+-----+-----+ 360
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA
361 -----+-----+-----+-----+-----+-----+-----+ 420
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
421 -----+-----+-----+-----+-----+-----+-----+ 480
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
481 -----+-----+-----+-----+-----+-----+-----+ 540
TGTTCTTGGTCCAGTCGGAAGTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTG
541 -----+-----+-----+-----+-----+-----+-----+ 600
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -

FIG. 22B

```
601 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAG 660
-----+-----+-----+-----+-----+
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a      D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 720
-----+-----+-----+-----+-----+
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC 757
-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG

a      K S L S L S P G K *
```

FIG. 23A

NdeI
 |
 CATATGGACAAAACCTCACACATGTCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCG
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 GTATACCTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

TCAGTTTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
 61 -----+-----+-----+-----+-----+-----+-----+ 120
 AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
 121 -----+-----+-----+-----+-----+-----+-----+ 180
 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
 181 -----+-----+-----+-----+-----+-----+-----+ 240
 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC

a V D G V E V H N A K T K P R E E Q Y N S -

ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
 241 -----+-----+-----+-----+-----+-----+-----+ 300
 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCTCTC

a T Y R V V S V L T V L H Q D W L N G K E -

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
 301 -----+-----+-----+-----+-----+-----+-----+ 360
 ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
 361 -----+-----+-----+-----+-----+-----+-----+ 420
 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
 421 -----+-----+-----+-----+-----+-----+-----+ 480
 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
 481 -----+-----+-----+-----+-----+-----+-----+ 540
 CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCAGGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
 541 -----+-----+-----+-----+-----+-----+-----+ 600
 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 23B

```

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
-----+-----+-----+-----+-----+-----+
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGGTGAACCGAACTGTGAC 720
-----+-----+-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACCTGGCTTGACACTG

a      K  S  L  S  L  S  P  G  K  G  G  G  G  G  V  E  P  N  C  D  -

                                           BamHI
                                           |
721 ATCCATGTTATGTGGGAATGGGAATGTTTTGAACGTCTGTAACCTCGAGGATCC 773
-----+-----+-----+-----+-----+-----+
TAGGTACAATACACCCTTACCCTTACAAAACCTGCAGACATTGAGCTCCTAGG

a      I  H  V  M  W  E  W  E  C  F  E  R  L  *
```

FIG. 24A

NdeI
|
CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGT
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACCAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACCTTGCA

a M V E P N C D I H V M W E W E C F E R -

CTGGGTGGTGGTGGTGGTGACAAAACCTCACACATGTCCACCGTGCCCAGCACCTGAACTC
61 -----+-----+-----+-----+-----+-----+-----+ 120
GACCCACCACCACCACCCTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAG

a L G G G G G D K T H T C P P C P A P E L -

CTGGGGGGACCGTCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCC
121 -----+-----+-----+-----+-----+-----+-----+ 180
GACCCCCCTGGCAGTCAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGG

a L G G P S V F L F P P K P K D T L M I S -

CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG
181 -----+-----+-----+-----+-----+-----+-----+ 240
GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC

a R T P E V T C V V V D V S H E D P E V K -

TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG
241 -----+-----+-----+-----+-----+-----+-----+ 300
AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC

a F N W Y V D G V E V H N A K T K P R E E -

CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
301 -----+-----+-----+-----+-----+-----+-----+ 360
GTCATGTTGTGCGTGCATGGCACACCAAGTGCAGGAGTGGCAGGACGTGGTCTCTGACCGAC

a Q Y N S T Y R V V S V L T V L H Q D W L -

AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA
361 -----+-----+-----+-----+-----+-----+-----+ 420
TTACCGTTCCTCATGTTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT

a N G K E Y K C K V S N K A L P A P I E K -

ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
421 -----+-----+-----+-----+-----+-----+-----+ 480
TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG

a T I S K A K G Q P R E P Q V Y T L P P S -

CGGGATGAGCTGACCAAGAACCAGGTGACCTGCCTGGTCAAAGGCTTCTATCCC
481 -----+-----+-----+-----+-----+-----+-----+ 540
GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGG

a R D E L T K N Q V S L T C L V K G F Y P -

AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACG
541 -----+-----+-----+-----+-----+-----+-----+ 600
TCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGC

a S D I A V E W E S N G Q P E N N Y K T T -

FIG. 24B

```

CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG
601 -----+-----+-----+-----+-----+-----+ 660
GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTC
a      P P V L D S D G S F F L Y S K L T V D K -

AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC
661 -----+-----+-----+-----+-----+-----+ 720
TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG
a      S R W Q Q G N V F S C S V M H E A L H N -

                                     BamHI
                                     |
CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC
721 -----+-----+-----+-----+-----+-----+ 773
GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG
a      H Y T Q K S L S L S P G K *
```

FIG. 25A

NdeI
|
1 CATATGGACAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG
-----+-----+-----+-----+-----+-----+-----+-----+ 60
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

61 TCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
-----+-----+-----+-----+-----+-----+-----+-----+ 120
AGTCAGAAGGAGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
-----+-----+-----+-----+-----+-----+-----+-----+ 180
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
-----+-----+-----+-----+-----+-----+-----+-----+ 240
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC

a V D G V E V H N A K T K P R E E Q Y N S -

241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
-----+-----+-----+-----+-----+-----+-----+-----+ 300
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
-----+-----+-----+-----+-----+-----+-----+-----+ 360
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
-----+-----+-----+-----+-----+-----+-----+-----+ 420
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

421 ACCAAGAACCAGGTGAGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
-----+-----+-----+-----+-----+-----+-----+-----+ 480
TGGTTCCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
-----+-----+-----+-----+-----+-----+-----+-----+ 540
CACCTCACCTCTCGTTACCCGTGGCCTCTTGTGATGTTCTGGTGGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+-----+-----+-----+ 600
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 25B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
-----+-----+-----+-----+-----+-----+
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  .

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCACTGGGGT 720
-----+-----+-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA

A      K  S  L  S  L  S  P  G  K  G  G  G  G  G  C  T  T  H  W  G  .

          BamHI
          |
721 TTCACCCTGTGCTAATGGATCCCTCGAG 748
-----+-----+-----+-----+
AAGTGGGACACGATTACCTAGGGAGCTC

a      F  T  L  C  *
```

FIG. 26A

FIG. 26B

```

601 GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC GTGGACAAGAGCAGG 660
    +-----+-----+-----+-----+-----+
    CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCC
a   V L D S D G S F F L Y S K L T V D K S R .

    TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
661 +-----+-----+-----+-----+-----+ 720
    ACCGTCGTCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG
a   W Q Q G N V F S C S V M H E A L H N H Y .

                                BamHI
                                |
    ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721 +-----+-----+-----+-----+-----+ 763
    TCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a   T Q K S L S L S P G K *
```